

10/581008

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SEQUENCE LISTING

<110> Takeda Pharmaceutical Company Limited
<120> Method of Estimating Toxicity of Drug
<130> 09707
<150> JP 2003-397551
<151> 2003-11-27

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<170> Patentin version 3.2

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Thr Ile Cys Thr Ser Ile Val Ala Glu Asp Lys Lys Gly His Leu Ile
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agg aca ccc atg agc gta gag atc aaa ggg aag aac gaa gag ctc atc Arg Thr Pro Met Ser Val Glu Ile Lys Gly Lys Asn Glu Glu Leu Ile 85 90 95	764
cgt gag ata gca ggc ttg gtg aga cgc tat gac cgt aat gaa atc acc Arg Glu Ile Ala Gly Leu Val Arg Arg Tyr Asp Arg Asn Glu Ile Thr 100 105 110	812
atc tgg gcc tcg gag aag agc tcg gtc atg aag aaa tgc aag gct gcc Ile Trp Ala Ser Glu Lys Ser Ser Val Met Lys Lys Cys Lys Ala Ala 115 120 125	860
aac ccc gag atg ccc ctg tcc ttc aca ata agc cga gga ttc tgg gtg Asn Pro Glu Met Pro Leu Ser Phe Thr Ile Ser Arg Gly Phe Trp Val 130 135 140 145	908
ctg ctt tcc tac tac ctg ggg ctg ctg ccc ttc atc cca atc cct gag Leu Leu Ser Tyr Tyr Leu Leu Pro Phe Ile Pro Ile Pro Glu 150 155 160	956
aag ttc ttc ttc tgc ttc ctg ccc aac atc atc aac agg acc tat ttc Lys Phe Phe Cys Phe Leu Pro Asn Ile Ile Asn Arg Thr Tyr Phe 165 170 175	1004
cca ttt tcc tgc tct tgc ctg aac cag tta ttg gct gtg gtt tcg aaa Pro Phe Ser Cys Ser Cys Leu Asn Gln Leu Leu Ala Val Val Ser Lys 180 185 190	1052
tgg ctg atc atg agg aag agt ctg atc cga cac ttg gag gag cga ggg Trp Leu Ile Met Arg Lys Ser Leu Ile Arg His Leu Glu Glu Arg Gly 195 200 205	1100
gtg cag gtg gtc ttt tgg tgc ctt aat gaa gag tgc gat ttt gaa gca Val Gln Val Val Phe Trp Cys Leu Asn Glu Glu Ser Asp Phe Glu Ala 210 215 220 225	1148
gcc ttc agc gtg gga gcc act ggc gtc ata acg gat tat ccc aca gcc Ala Phe Ser Val Gly Ala Thr Gly Val Ile Thr Asp Tyr Pro Thr Ala 230 235 240	1196
ctg cgg cac tac ctg gac aac cat gga cca gct gcc cgg acc tcc Leu Arg His Tyr Leu Asp Asn His Gly Pro Ala Ala Arg Thr Ser 245 250 255	1241
taagtccaga agcctcgagg tcttcgttt ctttcctga aaaataaata tttgccttc	1301
gatcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa	1336

<210> 6
<211> 256
<212> PRT
<213> Homo sapiens

<400> 6

Met Ala Gln Arg Ser Asp Leu Leu Glu Leu Asp Cys Gln Leu Thr Arg
1 5 10 15

Asp Arg Val Val Val Val Ser His Asp Glu Asn Leu Cys Arg Gln Ser
20 25 30

Gly Leu Asn Arg Asp Val Gly Ser Leu Asp Phe Glu Asp Leu Pro Leu
35 40 45

Tyr Lys Glu Lys Leu Glu Val Tyr Phe Ser Pro Gly His Phe Ala His
50 55 60

Gly Ser Asp Arg Arg Met Val Arg Leu Glu Asp Leu Phe Gln Arg Phe
65 70 75 80

Pro Arg Thr Pro Met Ser Val Glu Ile Lys Gly Lys Asn Glu Glu Leu
85 90 95

Ile Arg Glu Ile Ala Gly Leu Val Arg Arg Tyr Asp Arg Asn Glu Ile
100 105 110

Thr Ile Trp Ala Ser Glu Lys Ser Ser Val Met Lys Lys Cys Lys Ala
115 120 125

Ala Asn Pro Glu Met Pro Leu Ser Phe Thr Ile Ser Arg Gly Phe Trp
130 135 140

Val Leu Leu Ser Tyr Tyr Leu Gly Leu Leu Pro Phe Ile Pro Ile Pro
145 150 155 160

Glu Lys Phe Phe Cys Phe Leu Pro Asn Ile Ile Asn Arg Thr Tyr
165 170 175

Phe Pro Phe Ser Cys Ser Cys Leu Asn Gln Leu Leu Ala Val Val Ser
180 185 190

Lys Trp Leu Ile Met Arg Lys Ser Leu Ile Arg His Leu Glu Glu Arg
195 200 205

Gly Val Gln Val Val Phe Trp Cys Leu Asn Glu Glu Ser Asp Phe Glu
210 215 220

Ala Ala Phe Ser Val Gly Ala Thr Gly Val Ile Thr Asp Tyr Pro Thr
225 230 235 240

Ala Leu Arg His Tyr Leu Asp Asn His Gly Pro Ala Ala Arg Thr Ser
245 250 255

<210> 7
<211> 2631
<212> DNA
<213> Homo sapiens

<220>
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Met Thr Glu Gly Thr Cys Leu Arg Arg Arg Gly
1 5 10

ggc ccc tac aag acc gag ccc gcc acc gac ctc ggc cgc tgg cga ctc 99
Gly Pro Tyr Lys Thr Glu Pro Ala Thr Asp Leu Gly Arg Trp Arg Leu
15 20 25

aac tgc gag agg ggc cgg cag acg tgg acc tac ctg cag gac gag cgc Asn Cys Glu Arg Gly Arg Gln Thr Trp Thr Tyr Leu Gln Asp Glu Arg 30 35 40	147
gcc ggc cgc gag cag acc ggc ctg gaa gcc tac gcc ctg ggg ctg gac Ala Gly Arg Glu Gln Thr Gly Leu Glu Ala Tyr Ala Leu Gly Leu Asp 45 50 55	195
acc aag aat tac ttt aag gac ttg ccc aaa gcc cac acc gcc ttt gag Thr Lys Asn Tyr Phe Lys Asp Leu Pro Lys Ala His Thr Ala Phe Glu 60 65 70 75	243
ggg gct ctg aac ggg atg aca ttt tac gtg ggg ctg cag gct gag gat Gly Ala Leu Asn Gly Met Thr Phe Tyr Val Gly Leu Gln Ala Glu Asp 80 85 90	291
ggg cac tgg acg ggt gat tat ggt ggc cca ctt ttc ctc ctg cca ggc Gly His Trp Thr Gly Asp Tyr Gly Gly Pro Leu Phe Leu Leu Pro Gly 95 100 105	339
ctc ctg atc act tgc cac gtg gca cgc atc cct ctg cca gcc gga tac Leu Leu Ile Thr Cys His Val Ala Arg Ile Pro Leu Pro Ala Gly Tyr 110 115 120	387
aga gaa gag att gtg cgg tac ctg cgg tca gtg cag ctc cct gac ggt Arg Glu Ile Val Arg Tyr Leu Arg Ser Val Gln Leu Pro Asp Gly 125 130 135	435
ggc tgg ggc ctg cac att gag gat aag tcc acc gtg ttt ggg act gcg Gly Trp Gly Leu His Ile Glu Asp Lys Ser Thr Val Phe Gly Thr Ala 140 145 150 155	483
ctc aac tat gtg tct ctc aga att ctg ggt gtt ggg cct gac gat cct Leu Asn Tyr Val Ser Leu Arg Ile Leu Gly Val Gly Pro Asp Asp Pro 160 165 170	531
gac ctg gta cga gcc cgg aac att ctt cac aag aaa ggt ggt gct gtg Asp Leu Val Arg Ala Arg Asn Ile Leu His Lys Lys Gly Gly Ala Val 175 180 185	579
gcc atc ccc tcc tgg ggg aag ttc tgg ctg got gtc ctg aat gtt tac Ala Ile Pro Ser Trp Gly Lys Phe Trp Leu Ala Val Leu Asn Val Tyr 190 195 200	627
agc tgg gaa ggc ctc aat acc ctg ttc cca gag atg tgg ctg ttt cct Ser Trp Glu Gly Leu Asn Thr Leu Phe Pro Glu Met Trp Leu Phe Pro 205 210 215	675
gac tgg gca ccg gca cac ccc tcc aca ctc tgg tgc cac tgc cgg cag Asp Trp Ala Pro Ala His Pro Ser Thr Leu Trp Cys His Cys Arg Gln 220 225 230 235	723
gtg tac ctg ccc atg agc tac tgc tac gcc gtt cgg ctg agt gcc gcg Val Tyr Leu Pro Met Ser Tyr Cys Tyr Ala Val Arg Leu Ser Ala Ala 240 245 250	771
gaa gac ccg ctg gtc cag agc ctc cgc cag gag ctc tat gtg gag gac Glu Asp Pro Leu Val Gln Ser Leu Arg Gln Glu Leu Tyr Val Glu Asp 255 260 265	819
ttc gcc agc att gac tgg ctg gcg cag agg aac aac gtg gcc ccc gac Phe Ala Ser Ile Asp Trp Leu Ala Gln Arg Asn Asn Val Ala Pro Asp 270 275 280	867
gag ctg tac acg ccg cac agc tgg ctg ctc cgc gtg gta tat gct ctc Glu Leu Tyr Thr Pro His Ser Trp Leu Leu Arg Val Val Tyr Ala Leu 285 290 295	915
ctc aac ctg tat gag cac cac cac agt gcc cac ctg cgg cag cgg gcc Leu Asn Leu Tyr Gln His His Ser Ala His Leu Arg Gln Arg Ala 300 305 310 315	963
gtg cag aag ctg tat gaa cac att gtg gcc gac gac cga ttc acc aag Val Gln Lys Leu Tyr Glu His Ile Val Ala Asp Asp Arg Phe Thr Lys 320 325 330	1011

agc atc agc atc ggc ccg atc tcg aaa acc atc aac atg ctt gtg cgc Ser Ile Ser Ile Gly Pro Ile Ser Lys Thr Ile Asn Met Leu Val Arg 335 340 345	1059
tgg tat gtg gac ggg ccc gcc tcc act gcc ttc cag gag cat gtc tcc Trp Tyr Val Asp Gly Pro Ala Ser Thr Ala Phe Gln Glu His Val Ser 350 355 360	1107
aga atc ccg gac tat ctc tgg atg ggc ctt gac ggc atg aaa atg cag Arg Ile Pro Asp Tyr Leu Trp Met Gly Leu Asp Gly Met Lys Met Gln 365 370 375	1155
ggc acc aac ggc tca cag atc tgg gac acc gca ttc gcc atc cag gct Gly Thr Asn Gly Ser Gln Ile Trp Asp Thr Ala Phe Ala Ile Gln Ala 380 385 390 395	1203
ctg ctt gag gcg ggc ggg cac cac agg ccc gag ttt tcg tcc tgc ctg Leu Leu Glu Ala Gly Gly His His Arg Pro Glu Phe Ser Ser Cys Leu 400 405 410	1251
cag aag gct cat gag ttc ctg agg ctc tca cag gtc cca gat aac cct Gln Lys Ala His Glu Phe Leu Arg Leu Ser Gln Val Pro Asp Asn Pro 415 420 425	1299
ccc gac tac cag aag tac tac cgc cag atg cgc aag ggt ggc ttc tcc Pro Asp Tyr Gln Lys Tyr Tyr Arg Gln Met Arg Lys Gly Gly Phe Ser 430 435 440	1347
ttc agt acg ctg gac tgc ggc tgg atc gtt tct gac tgc acg gct gag Phe Ser Thr Leu Asp Cys Gly Trp Ile Val Ser Asp Cys Thr Ala Glu 445 450 455	1395
gcc ttg aag gct gtg ctg ctc ctg cag gag aag tgt ccc cat gtc acc Ala Leu Lys Ala Val Leu Leu Gln Glu Lys Cys Pro His Val Thr 460 465 470 475	1443
gag cac atc ccc aga gaa cgg ctc tgc gat gct gtg gct gtg ctg ctg Glu His Ile Pro Arg Glu Arg Leu Cys Asp Ala Val Ala Val Leu Leu 480 485 490	1491
aac atg aga aat cca gat gga ggg ttc gcc acc tat gag acc aag cgt Asn Met Arg Asn Pro Asp Gly Gly Phe Ala Thr Tyr Glu Thr Lys Arg 495 500 505	1539
ggg ggg cac ttg ctg gag ctg ctg aac ccc tgc gag gtc ttc ggg gac Gly Gly His Leu Leu Glu Leu Leu Asn Pro Ser Glu Val Phe Gly Asp 510 515 520	1587
atc atg att gac tac acc tat gtg gag tgc acc tca gcc gtg atg cag Ile Met Ile Asp Tyr Thr Tyr Val Glu Cys Thr Ser Ala Val Met Gln 525 530 535	1635
gcg ctt aag tat ttc cac aag cgt ttc ccg gag cac agg gca gcg gag Ala Leu Lys Tyr Phe His Lys Arg Phe Pro Glu His Arg Ala Ala Glu 540 545 550 555	1683
atc cgg gag acc ctc acg cag ggc tta gag ttc tgt cgg cgg cag cag Ile Arg Glu Thr Leu Thr Gln Gly Leu Glu Phe Cys Arg Arg Gln Gln 560 565 570	1731
agg gcc gat ggc tcc tgg gaa ggc tcc tgg gga gtt tgc ttc acc tac Arg Ala Asp Gly Ser Trp Glu Gly Ser Trp Gly Val Cys Phe Thr Tyr 575 580 585	1779
ggc acc tgg ttt ggc ctg gag gcc ttc gcc tgt atg ggg cag acc tac Gly Thr Trp Phe Gly Leu Glu Ala Phe Ala Cys Met Gly Gln Thr Tyr 590 595 600	1827
cga gat ggg act gcc tgt gca gag gtc tcc cgg gcc tgt gac ttc ctg Arg Asp Gly Thr Ala Cys Ala Glu Val Ser Arg Ala Cys Asp Phe Leu 605 610 615	1875
ctg tcc cgg cag atg gca gac gga ggc tgg ggg gag gac ttt gag tcc Leu Ser Arg Gln Met Ala Asp Gly Gly Trp Gly Glu Asp Phe Glu Ser 620 625 630 635	1923

tgc gag gag cgg cgt tat ttg cag agt gcc cag tcc cag atc cat aac Cys Glu Glu Arg Arg Tyr Leu Gln Ser Ala Gln Ser Gln Ile His Asn 640 645 650	1971
aca tgc tgg gcc atg atg ggg ctg atg gcc gtt cgg cat cct gac atc Thr Cys Trp Ala Met Met Gly Leu Met Ala Val Arg His Pro Asp Ile 655 660 665	2019
gag gcc cag gag aga gga gtc cgg tgt cta ctt gag aaa cag ctc ccc Glu Ala Gln Glu Arg Gly Val Arg Cys Leu Leu Glu Lys Gln Leu Pro 670 675 680	2067
aat ggc gac tgg ccg cag gaa aac att gct ggg gtc ttc aac aag tcc Asn Gly Asp Trp Pro Gln Glu Asn Ile Ala Gly Val Phe Asn Lys Ser 685 690 695	2115
tgt gcc atc tcc tac acg agc tac agg aac atc ttc ccc atc tgg gcc Cys Ala Ile Ser Tyr Thr Ser Tyr Arg Asn Ile Phe Pro Ile Trp Ala 700 705 710 715	2163
ctc ggc cgc ttc tcc cag ctg tac cct gag aga gcc ctt gct ggc cac Leu Gly Arg Phe Ser Gln Leu Tyr Pro Glu Arg Ala Leu Ala Gly His 720 725 730	2211
ccc tgagaacatg cctaccgtct ggggccgtc tgtgcgttcc atggccttca Pro	2264
agtcacagga cgacgcgatt ccctgccttc ttccgggttta ttacacaggc aggacttcag tgtcagtatc cctgccttca gtcttcttta gaaatcacat ctgtgttcaa tccattgttt agagggagtg tattttcct gttccacgaa gaggacttt tgttcacaat tggatcacaa tgcagaggag tctgttccct ccccgctggc ttctccgtgc tgggagggtg acctgtccca gtgactcat caccctgaca tgctcttgac aaaggacacc accaagagga gatggcagct gtaccgggtgc agcctctgtc tgagggggat atttgctca gtgtgattaa aaatcagtca tgaaaga	2324 2384 2444 2504 2564 2624 2631

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<211> 732
<212> PRT
<213> Homo sapiens

<400> 8

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Glu Pro Ala Thr Asp Leu Gly Arg Trp Arg Leu Asn Cys Glu Arg Gly
20 25 30

Arg Gln Thr Trp Thr Tyr Leu Gln Asp Glu Arg Ala Gly Arg Glu Gln
35 40 45

Thr Gly Leu Glu Ala Tyr Ala Leu Gly Leu Asp Thr Lys Asn Tyr Phe
50 55 60

Lys Asp Leu Pro Lys Ala His Thr Ala Phe Glu Gly Ala Leu Asn Gly
65 70 75 80

Met Thr Phe Tyr Val Gly Leu Gln Ala Glu Asp Gly His Trp Thr Gly
85 90 95

Asp Tyr Gly Gly Pro Leu Phe Leu Leu Pro Gly Leu Leu Ile Thr Cys
100 105 110

His Val Ala Arg Ile Pro Leu Pro Ala Gly Tyr Arg Glu Glu Ile Val
115 120 125

Arg Tyr Leu Arg Ser Val Gln Leu Pro Asp Gly Gly Trp Gly Leu His
130 135 140

Ile Glu Asp Lys Ser Thr Val Phe Gly Thr Ala Leu Asn Tyr Val Ser
145 150 155 160

Leu Arg Ile Leu Gly Val Gly Pro Asp Asp Pro Asp Leu Val Arg Ala
165 170 175

Arg Asn Ile Leu His Lys Lys Gly Gly Ala Val Ala Ile Pro Ser Trp
180 185 190

Gly Lys Phe Trp Leu Ala Val Leu Asn Val Tyr Ser Trp Glu Gly Leu
195 200 205

Asn Thr Leu Phe Pro Glu Met Trp Leu Phe Pro Asp Trp Ala Pro Ala
210 215 220

His Pro Ser Thr Leu Trp Cys His Cys Arg Gln Val Tyr Leu Pro Met
225 230 235 240

Ser Tyr Cys Tyr Ala Val Arg Leu Ser Ala Ala Glu Asp Pro Leu Val
245 250 255

Gln Ser Leu Arg Gln Glu Leu Tyr Val Glu Asp Phe Ala Ser Ile Asp
260 265 270

Trp Leu Ala Gln Arg Asn Asn Val Ala Pro Asp Glu Leu Tyr Thr Pro
275 280 285

His Ser Trp Leu Leu Arg Val Val Tyr Ala Leu Leu Asn Leu Tyr Glu
290 295 300

His His His Ser Ala His Leu Arg Gln Arg Ala Val Gln Lys Leu Tyr
305 310 315 320

Glu His Ile Val Ala Asp Asp Arg Phe Thr Lys Ser Ile Ser Ile Gly
325 330 335

Pro Ile Ser Lys Thr Ile Asn Met Leu Val Arg Trp Tyr Val Asp Gly
340 345 350

Pro Ala Ser Thr Ala Phe Gln Glu His Val Ser Arg Ile Pro Asp Tyr
355 360 365

Leu Trp Met Gly Leu Asp Gly Met Lys Met Gln Gly Thr Asn Gly Ser
370 375 380

Gln Ile Trp Asp Thr Ala Phe Ala Ile Gln Ala Leu Leu Glu Ala Gly
385 390 395 400

Gly His His Arg Pro Glu Phe Ser Ser Cys Leu Gln Lys Ala His Glu
405 410 415

Phe Leu Arg Leu Ser Gln Val Pro Asp Asn Pro Pro Asp Tyr Gln Lys
420 425 430

Tyr Tyr Arg Gln Met Arg Lys Gly Gly Phe Ser Phe Ser Thr Leu Asp
435 440 445

Cys Gly Trp Ile Val Ser Asp Cys Thr Ala Glu Ala Leu Lys Ala Val
450 455 460

Leu Leu Leu Gln Glu Lys Cys Pro His Val Thr Glu His Ile Pro Arg
465 470 475 480

Glu Arg Leu Cys Asp Ala Val Ala Val Leu Leu Asn Met Arg Asn Pro
485 490 495

Asp Gly Gly Phe Ala Thr Tyr Glu Thr Lys Arg Gly Gly His Leu Leu
500 505 510

Glu Leu Leu Asn Pro Ser Glu Val Phe Gly Asp Ile Met Ile Asp Tyr
515 520 525

Thr Tyr Val Glu Cys Thr Ser Ala Val Met Gln Ala Leu Lys Tyr Phe
530 535 540

His Lys Arg Phe Pro Glu His Arg Ala Ala Glu Ile Arg Glu Thr Leu
545 550 555 560

Thr Gln Gly Leu Glu Phe Cys Arg Arg Gln Gln Arg Ala Asp Gly Ser
565 570 575

Trp Glu Gly Ser Trp Gly Val Cys Phe Thr Tyr Gly Thr Trp Phe Gly
580 585 590

Leu Glu Ala Phe Ala Cys Met Gly Gln Thr Tyr Arg Asp Gly Thr Ala
595 600 605

Cys Ala Glu Val Ser Arg Ala Cys Asp Phe Leu Leu Ser Arg Gln Met
610 615 620

Ala Asp Gly Gly Trp Gly Glu Asp Phe Glu Ser Cys Glu Glu Arg Arg
625 630 635 640

Tyr Leu Gln Ser Ala Gln Ser Gln Ile His Asn Thr Cys Trp Ala Met
645 650 655

Met Gly Leu Met Ala Val Arg His Pro Asp Ile Glu Ala Gln Glu Arg
660 665 670

Gly Val Arg Cys Leu Leu Glu Lys Gln Leu Pro Asn Gly Asp Trp Pro
675 680 685

Gln Glu Asn Ile Ala Gly Val Phe Asn Lys Ser Cys Ala Ile Ser Tyr
690 695 700

Thr Ser Tyr Arg Asn Ile Phe Pro Ile Trp Ala Leu Gly Arg Phe Ser
705 710 715 720

Gln Leu Tyr Pro Glu Arg Ala Leu Ala Gly His Pro
725 730

<210> 9
<211> 1168
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (30)..(800)

<400> 9
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1 5
tgc cca tgc cag gga gct gca agc cgc ccc gcc att ctc tac gca ctt 101
Cys Pro Cys Gln Gly Ala Ala Ser Arg Pro Ala Ile Leu Tyr Ala Leu
10 15 20
ctg agc tcc agc ctc aag gct gtc ccc cga ccc cgt agc cgc tgc cta 149
Leu Ser Ser Leu Lys Ala Val Pro Arg Pro Arg Ser Arg Cys Leu
25 30 35 40
tgt agg cag cac cgg ccc gtc cag cta tgt gca cct cat cgc acc tgc 197
Cys Arg Gln His Arg Pro Val Gln Leu Cys Ala Pro His Arg Thr Cys
45 50 55
cggttggatgttctggccaaaggacaatgtggccttctcaggaac 245
Arg Glu Ala Leu Asp Val Leu Ala Lys Thr Val Ala Phe Leu Arg Asn
60 65 70
ctg cca tcc ttc tgg cag ctg ccc cag gag cgg cgg ctg ctg 293
Leu Pro Ser Phe Trp Gln Leu Pro Pro Gln Asp Gln Arg Arg Leu Leu
75 80 85
cag ggt tgc tgg ggc ccc ctc ttc ctg ctt ggg ttg gcc caa gat gct 341
Gln Gly Cys Trp Gly Pro Leu Phe Leu Leu Gly Leu Ala Gln Asp Ala
90 95 100
gtg acc ttt gag gtg gct gag gcc ccg gtg ccc agc ata ctc aag aag 389
Val Thr Phe Glu Val Ala Glu Ala Pro Val Pro Ser Ile Leu Lys Lys
105 110 115 120
att ctg ctg gag gag ccc agc agc agt gga ggc agt ggc caa ctg cca 437
Ile Leu Leu Glu Glu Pro Ser Ser Ser Gly Gly Ser Gly Gln Leu Pro
125 130 135
gac aga ccc cag ccc tcc ctg gct ggc gtg cag tgg ctt caa tgc tgt 485
Asp Arg Pro Gln Pro Ser Leu Ala Ala Val Gln Trp Leu Gln Cys Cys
140 145 150
ctg gag tcc ttc tgg agc ctg gag ctt agc ccc aag gaa tat gcc tgc 533
Leu Glu Ser Phe Trp Ser Leu Glu Leu Ser Pro Lys Glu Tyr Ala Cys
155 160 165
ctg aaa ggg acc atc ctc ttc aac ccc gat gtg cca ggc ctc caa gcc 581
Leu Lys Gly Thr Ile Leu Phe Asn Pro Asp Val Pro Gly Leu Gln Ala
170 175 180
gcc tcc cac att ggg cac ctg cag gag gct cac tgg gtg ctg tgt 629
Ala Ser His Ile Gly His Leu Gln Gln Glu Ala His Trp Val Leu Cys
185 190 195 200
gaa gtc ctg gaa ccc tgg tgc cca gca gcc caa ggc cgc ctg acc cgt 677
Glu Val Leu Glu Pro Trp Cys Pro Ala Ala Gln Gly Arg Leu Thr Arg
205 210 215
gtc ctc ctc acg gcc tcc acc ctc aag tcc att ccg acc agc ctg ctt 725
Val Leu Leu Thr Ala Ser Thr Leu Lys Ser Ile Pro Thr Ser Leu Leu
220 225 230

ggg gac ctc ttc ttt cgc cct atc att gga gat gtt gac atc gct ggc	773
Gly Asp Leu Phe Phe Arg Pro Ile Ile Gly Asp Val Asp Ile Ala Gly	
235 240 245	
ctt ctt ggg gac atg ctt ttg ctc agg tgacctgttc cagcccccaggc	820
Leu Leu Gly Asp Met Leu Leu Leu Arg	
250 255	
agagatcagg tggcagagg ctggcagtgc tgattcagcc tggccatccc cagaggtgac	880
ccaatgcgcc tggggggca agcctgtata gacagcactt ggctccttag gaacagctct	940
tcactcagcc acaccccaaca ttggacttcc ttgggttgga cacagtgcctc cagctgcctg	1000
ggaggctttt ggtggcccccc acagcctctg ggccaagact cctgtccctt ctggatga	1060
gaatgaaagc ttaggctgtt tattggacca gaagtccatat cgactttata cagaactgaa	1120
ttaagttatt gatTTTgtA ataaaaggta tgaacacta aaaaaaaaa	1168

<210> 10
<211> 257
<212> PRT
<213> Homo sapiens

<400> 10

Met Ser Thr Ser Gln Pro Gly Ala Cys Pro Cys Gln Gly Ala Ala Ser
1 5 10 15

Arg Pro Ala Ile Leu Tyr Ala Leu Leu Ser Ser Ser Leu Lys Ala Val
20 25 30

Pro Arg Pro Arg Ser Arg Cys Leu Cys Arg Gln His Arg Pro Val Gln
35 40 45

Leu Cys Ala Pro His Arg Thr Cys Arg Glu Ala Leu Asp Val Leu Ala
50 55 60

Lys Thr Val Ala Phe Leu Arg Asn Leu Pro Ser Phe Trp Gln Leu Pro
65 70 75 80

Pro Gln Asp Gln Arg Arg Leu Leu Gln Gly Cys Trp Gly Pro Leu Phe
85 90 95

Leu Leu Gly Leu Ala Gln Asp Ala Val Thr Phe Glu Val Ala Glu Ala
100 105 110

Pro Val Pro Ser Ile Leu Lys Ile Leu Leu Glu Glu Pro Ser Ser
115 120 125

Ser Gly Gly Ser Gly Gln Leu Pro Asp Arg Pro Gln Pro Ser Leu Ala
130 135 140

Ala Val Gln Trp Leu Gln Cys Cys Leu Glu Ser Phe Trp Ser Leu Glu
145 150 155 160

Leu Ser Pro Lys Glu Tyr Ala Cys Leu Lys Gly Thr Ile Leu Phe Asn
165 170 175

Pro Asp Val Pro Gly Leu Gln Ala Ala Ser His Ile Gly His Leu Gln
180 185 190

Gln Glu Ala His Trp Val Leu Cys Glu Val Leu Glu Pro Trp Cys Pro
195 200 205

Ala Ala Gln Gly Arg Leu Thr Arg Val Leu Leu Thr Ala Ser Thr Leu
210 215 220

Lys Ser Ile Pro Thr Ser Leu Leu Gly Asp Leu Phe Phe Arg Pro Ile
225 230 235 240

Ile Gly Asp Val Asp Ile Ala Gly Leu Leu Gly Asp Met Leu Leu Leu
245 250 255

Arg

<210> 11
<211> 489
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (43)...(423)

<400> 11
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Met Ser Phe Ser
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ggc aag tac caa ctg cag agc cag gaa aac ttt gaa gcc ttc atg aag 102
Gly Lys Tyr Gln Leu Gln Ser Gln Glu Asn Phe Glu Ala Phe Met Lys
5 10 15 20

gca atc ggt ctg ccg gaa gag ctc atc cag aag ggg aag gat atc aag 150
Ala Ile Gly Leu Pro Glu Glu Leu Ile Gln Lys Gly Lys Asp Ile Lys
25 30 35

ggg gtg tcg gaa atc gtg cag aat ggg aag cac ttc aag ttc acc atc 198
Gly Val Ser Glu Ile Val Gln Asn Gly Lys His Phe Lys Phe Thr Ile
40 45 50

acc gct ggg tcc aaa gtg atc caa aac gaa ttc acg gtg egg gag gaa 246
Thr Ala Gly Ser Lys Val Ile Gln Asn Glu Phe Thr Val Gly Glu Glu
55 60 65

tgt gag ctg gag aca atg aca ggg gag aaa gtc aag aca gtg gtt cag 294
Cys Glu Leu Glu Thr Met Thr Gly Glu Lys Val Lys Thr Val Val Gln
70 75 80

ttg gaa ggt gac aat aaa ctg gtg aca act ttc aaa aac atc aag tct 342
Leu Glu Gly Asp Asn Lys Leu Val Thr Thr Phe Lys Asn Ile Lys Ser
85 90 95 100

gtg acc gaa ctc aac ggc gac ata atc acc aat acc atg aca ttg ggt 390
Val Thr Glu Leu Asn Gly Asp Ile Ile Thr Asn Thr Met Thr Leu Gly
105 110 115

gac att gtc ttc aag aga atc agc aag aga att taaacaagtc tgcattcat 443
Asp Ile Val Phe Lys Arg Ile Ser Lys Arg Ile
120 125

attatTTTGTGTAAAT TAATGTATAA AAGTGAACTT TGTGGT 489

<210> 12
<211> 127
<212> PRT
<213> Homo sapiens

<400> 12

Met Ser Phe Ser Gly Lys Tyr Gln Leu Gln Ser Gln Glu Asn Phe Glu
1 5 10 15

Ala Phe Met Lys Ala Ile Gly Leu Pro Glu Glu Leu Ile Gln Lys Gly
20 25 30

Lys Asp Ile Lys Gly Val Ser Glu Ile Val Gln Asn Gly Lys His Phe
35 40 45

Lys Phe Thr Ile Thr Ala Gly Ser Lys Val Ile Gln Asn Glu Phe Thr
50 55 60

Val Gly Glu Glu Cys Glu Leu Glu Thr Met Thr Gly Glu Lys Val Lys
65 70 75 80

Thr Val Val Gln Leu Glu Gly Asp Asn Lys Leu Val Thr Thr Phe Lys
85 90 95

Asn Ile Lys Ser Val Thr Glu Leu Asn Gly Asp Ile Ile Thr Asn Thr
100 105 110

Met Thr Leu Gly Asp Ile Val Phe Lys Arg Ile Ser Lys Arg Ile
115 120 125

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tgcccaggcc tggagactga cccgaccccg gcactacctc gaggctccgc ccccacctgc 180
tggaccccgag ggtcccaccc tggcccaggaa ggtcagccag ggaatcatta acaagaggca 240
gtgac atg ggc cag aag gag ggt ggc cgg act gtg cca tgc tgc tcc 287
Met Ala Gln Lys Glu Gly Gly Arg Thr Val Pro Cys Cys Ser
-160 -155 -150

aga ccc aag gtg gca gct ctc act ggc ggg acc ctg cta ctt ctg 332
Arg Pro Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu
-145 -140 -135

aca gcc atc ggg ggc gca tcc tgg gcc att gtg gct gtt ctc ctc 377
Thr Ala Ile Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu
-130 -125 -120

agg agt gac cag gag ccg ctg tac cca gtg cag gtc agc tct ggc 422
Arg Ser Asp Gln Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala
-115 -110 -105

gac gct cgg ctc atg gtc ttt gac aag acg gaa ggg acg tgg cgg ctg Asp Ala Arg Leu Met Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu -100 -95 -90	470
ctg tgc tcc tcg cgc tcc aac gcc agg gta gcc gga ctc agc tgc gag Leu Cys Ser Ser Arg Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu -85 -80 -75	518
gag atg ggc ttc ctc agg gca ctg acc cac tcc gag ctg gac gtg cga Glu Met Gly Phe Leu Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg -70 -65 -60	566
acg ggc ggc gcc aat ggc acg tcg ggc ttc ttc tgt gtg gac gag ggg Thr Ala Gly Ala Asn Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly -55 -50 -45 -40	614
agg ctg ccc cac acc cag agg ctg ctg gag gtc atc tcc gtg tgt gat Arg Leu Pro His Thr Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp -35 -30 -25	662
tgc ccc aga ggc cgt ttc ttg gcc gcc atc tgc caa gac tgt ggc cgc Cys Pro Arg Gly Arg Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg -20 -15 -10	710
agg aag ctg ccc gtc gac cgc atc gtg gga ggc cgg gac acc acc ttg Arg Lys Leu Pro Val Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu -5 -1 1 5	758
ggc cgg tgg ccg tgg caa gtc agc ctt cgc tat gat gga gca cac ctc Gly Arg Trp Pro Trp Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu 10 15 20 25	806
tgt ggg gga tcc ctg ctc tcc ggg gac tgg gtg ctg aca gcc gcc cac Cys Gly Gly Ser Leu Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His 30 35 40	854
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ggc gtc gtc gtc cag gcc tct ccc cac ggt ctg cag ctg ggg gtg cag Gly Ala Val Ala Gln Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln 60 65 70	950
gct gtg gtc tac cac ggg ggc tat ctt ccc ttt cgg gac ccc aac agc Ala Val Val Tyr His Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser 75 80 85	998
gag gag aac agc aac gat att gcc ctg gtc cac ctc tcc agt ccc ctg Glu Glu Asn Ser Asn Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu 90 95 100 105	1046
ccc ctc aca gaa tac atc cag cct gtg tgc ctc cca gct gcc ggc cag Pro Leu Thr Glu Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln 110 115 120	1094
gcc ctg gtg gat ggc aag atc tgt acc gtg acg ggc tgg ggc aac acg Ala Leu Val Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr 125 130 135	1142
cag tac tat ggc caa cag gcc ggg gta ctc cag gag gct cga gtc ccc Gln Tyr Tyr Gly Gln Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro 140 145 150	1190
ata atc agc aat gat gtc tgc aat ggc gct gac ttc tat gga aac cag Ile Ile Ser Asn Asp Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln 155 160 165	1238
atc aag ccc aag atg ttc tgt gct ggc tac ccc gag ggt ggc att gat Ile Lys Pro Lys Met Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp 170 175 180 185	1286
gcc tgc cag ggc gac agc ggt ggt ccc ttt gtg tgt gag gac agc atc Ala Cys Gln Gly Asp Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile 190 195 200	1334

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Ser	Arg	Thr	Pro	Arg	Trp	Arg	Leu	Cys	Gly	Ile	Val	Ser	Trp	Gly	Thr		
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ggc	tgt	gcc	ctg	gcc	cag	aag	cca	ggc	gtc	tac	acc	aaa	gtc	agt	gac		1430
Gly	Cys	Ala	Leu	Ala	Gln	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Asp		
220					225					230							
ttc	cgg	gag	tgg	atc	tcc	cag	gcc	ata	aag	act	cac	tcc	gaa	gcc	agc		1478
Phe	Arg	Glu	Trp	Ile	Phe	Gln	Ala	Ile	Lys	Thr	His	Ser	Glu	Ala	Ser		
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Gly	Met	Val	Thr	Gln	Leu												
250					255												
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Pro Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu Leu Thr
-145 -140 -135

Ala Ile Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg
-130 -125 -120

Ser Asp Gln Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp
-115 -110 -105

Ala Arg Leu Met Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu
-100 -95 -90

Cys Ser Ser Arg Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu
-85 -80 -75

Met Gly Phe Leu Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr
-70 -65 -60 -55

Ala Gly Ala Asn Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg
-50 -45 -40

Leu Pro His Thr Gin Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys
-35 -30 -25

Pro Arg Gly Arg Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg
-20 -15 -10

Lys Leu Pro Val Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly

-5

-1 1

5

10

Arg Trp Pro Trp Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys
15 20 25

Gly Gly Ser Leu Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys
30 35 40

Phe Pro Glu Arg Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly
45 50 55

Ala Val Ala Gln Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala
60 65 70

Val Val Tyr His Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu
75 80 85 90

Glu Asn Ser Asn Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro
95 100 105

Leu Thr Glu Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gln Ala
110 115 120

Leu Val Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln
125 130 135

Tyr Tyr Gly Gln Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile
140 145 150

Ile Ser Asn Asp Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln Ile
155 160 165 170

Lys Pro Lys Met Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp Ala
175 180 185

Cys Gln Gly Asp Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile Ser
190 195 200

Arg Thr Pro Arg Trp Arg Leu Cys Gly Ile Val Ser Trp Gly Thr Gly
205 210 215

Cys Ala Leu Ala Gln Lys Pro Gly Val Tyr Thr Lys Val Ser Asp Phe
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235 240 245 250

Met Val Thr Gln Leu
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Leu Gly Leu Leu Ala Ala Gly Phe Cys Pro Ala Val Leu Cys His Pro
-15 -10 -5 -1

aac agc cca ctt gac gag aat ctg acc cag gag aac caa gac cga 148
Asn Ser Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg
1 5 10 15

ggg aca cac gtg gac ctc gga tta gcc tcc gcc aac gtg gac ttc gct 196
Gly Thr His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala
20 25 30

ttc agg ctg tac aag cag tta gtc ctg aag gcc ctt gat aag aat gtc 244
Phe Ser Leu Tyr Lys Gin Leu Val Leu Lys Ala Leu Asp Lys Asn Val
35 40 45

atc ttc tcc cca ctg agc atc tcc acc gcc ttg gcc ttc ctg tct ctg 292
Ile Phe Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu
50 55 60

ggg gcc cat aat acc acc ctg aca gag att ctc aag gcc tcg agt tca 340
Gly Ala His Asn Thr Thr Leu Thr Glu Ile Leu Lys Ala Ser Ser Ser
65 70 75 80

cct cac gga gac tta ctg agg cag aaa ttc act cag agc ttc cag cac 388
Pro His Gly Asp Leu Leu Arg Gin Lys Phe Thr Gin Ser Phe Gin His
85 90 95

ctc cgc gca ccc tca atc agt tcc agc gat gag ctg cag ctg agt atg 436
Leu Arg Ala Pro Ser Ile Ser Ser Asp Glu Leu Gin Leu Ser Met
100 105 110

gga aat gcc atg ttt gtc aaa gag caa ctc agt ctg ctg gac agg ttc 484
Gly Asn Ala Met Phe Val Lys Glu Gin Leu Ser Leu Leu Asp Arg Phe
115 120 125

acg gag gat gcc aag agg ctg tat ggc tcc gag gcc ttt gcc act gac 532
Thr Glu Asp Ala Lys Arg Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp
130 135 140

ttt cag gac tca gct gca gct aag aag ctc atc aac gac tac gtg aag 580
Phe Gin Asp Ser Ala Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys
145 150 155 160

aat gga act agg ggg aaa atc aca gat ctg atc aag gac ccc gac tcg 628
Asn Gly Thr Arg Gly Lys Ile Thr Asp Leu Ile Lys Asp Pro Asp Ser
165 170 175

cag aca atg atg gtc ctg gtg aat tac atc ttc ttt aaa gcc aaa tgg 676
Gin Thr Met Met Val Leu Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp
180 185 190

gag atg ccc ttt gac ccc caa gat act cat cag tca agg ttc tac ttg 724
Glu Met Pro Phe Asp Pro Gin Asp Thr His Gln Ser Arg Phe Tyr Leu
195 200 205

agc aag aaa aag tgg gta atg gtg ccc atg atg agt ttg cat cac ctg 772
Ser Lys Lys Trp Val Met Val Pro Met Met Ser Leu His His Leu
210 215 220

act ata cct tac ttc cgg gac gag gag ctg tcc tgc acc gtg gtg gag 820
Thr Ile Pro Tyr Phe Arg Asp Glu Glu Leu Ser Cys Thr Val Val Glu

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gac aag atg gag gaa gtg gaa gcc atg ctg ctc cca gag acc ctg aag Asp Lys Met Glu Glu Val Glu Ala Met Leu Leu Pro Glu Thr Leu Lys 260 265 270				916
cggtggaga gac tct ctg gag ttc aga gag ata ggt gag ctc tac ctg Arg Trp Arg Asp Ser Leu Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu 275 280 285				964
cca aag ttt tcc atc tcg agg gac tat aac ctg aac gac ata ctt ctc Pro Lys Phe Ser Ile Ser Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu 290 295 300				1012
cag ctg ggc att gag gaa gcc ttc acc agc aag gct gac ctg tca ggg Gln Leu Gly Ile Glu Glu Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly 305 310 315 320				1060
atc aca ggg gcc agg aac cta gca gtc tcc cag gtg gtc cat aag gtc Ile Thr Gly Ala Arg Asn Leu Ala Val Ser Gln Val Val His Lys Val 325 330 335				1108
gtg tct gat gta ttt gag gag ggc aca gaa gca tct gct gcc aca gca Val Ser Asp Val Phe Glu Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala 340 345 350				1156
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cgt ttc aac agg ccc ttc ctg atg atc att gtc cct aca gac acc cag Arg Phe Asn Arg Pro Phe Leu Met Ile Ile Val Pro Thr Asp Thr Gln 370 375 380				1252
aac atc ttc ttc atg agc aaa gtc acc aat ccc agc aag cct aga gct Asn Ile Phe Phe Met Ser Lys Val Thr Asn Pro Ser Lys Pro Arg Ala 385 390 395 400				1300
tgc atc aag cag tgg ggc tct cag taaggaactt ggaatgcaag ctggatgcct Cys Ile Lys Gln Trp Gly Ser Gln 405				1354
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<211> 433
<212> PRT
<213> Homo sapiens
<400> 16

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Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu Glu
-5 -1 1 5

Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr His Val Asp Leu Gly
10 15 20

Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser Leu Tyr Lys Gln Leu
25 30 35

Val Leu Lys Ala Leu Asp Lys Asn Val Ile Phe Ser Pro Leu Ser Ile
 40 45 50 55

Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr Leu
 60 65 70

Thr Glu Ile Leu Lys Ala Ser Ser Pro His Gly Asp Leu Leu Arg
 75 80 85

Gln Lys Phe Thr Gln Ser Phe Gln His Leu Arg Ala Pro Ser Ile Ser
 90 95 100

Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val Lys
 105 110 115

Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg Leu
 120 125 130 135

Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala Ala
 140 145 150

Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys Ile
 155 160 165

Thr Asp Leu Ile Lys Asp Pro Asp Ser Gln Thr Met Met Val Leu Val
 170 175 180

Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro Gln
 185 190 195

Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Trp Val Met
 200 205 210 215

Val Pro Met Met Ser Leu His His Leu Thr Ile Pro Tyr Phe Arg Asp
 220 225 230

Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys Tyr Thr Gly Asn Ala
 235 240 245

Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys Met Glu Glu Val Glu
 250 255 260

Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp Arg Asp Ser Leu Glu
 265 270 275

Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys Phe Ser Ile Ser Arg
 280 285 290 295

Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu Gly Ile Glu Glu Ala
 300 305 310

Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr Gly Ala Arg Asn Leu
 315 320 325

Ala Val Ser Gln Val Val His Lys Val Val Ser Asp Val Phe Glu Glu
 330 335 340

Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys Ile Thr Leu Leu Ser
345 350 355

Ala Leu Val Glu Thr Arg Thr Ile Val Arg Phe Asn Arg Pro Phe Leu
360 365 370 375

Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile Phe Phe Met Ser Lys
380 385 390

Val Thr Asn Pro Ser Lys Pro Arg Ala Cys Ile Lys Gln Trp Gly Ser
395 400 405

Gln

<210> 17
<211> 2008
<212> DNA
<213> Homo sapiens

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<222> (222)..(857)

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tccccaggggc ttccctttggaa ctggactgtc cctgtctatc cattctctcg ccaccccccag 180
acctccctcag ctccagggttg ccaccccttc tcgcccagagt g atg agg tcc cgg ctt 236
Met Arg Ser Arg Leu
1 5

ctg ctc tcc gtg gcc cat ctg ccc aca att cgg gag acc acg gag gag 284
Leu Leu Ser Val Ala His Leu Pro Thr Ile Arg Glu Thr Thr Glu Glu
10 15 20

atg ctg ctt ggg ggt cct gga cag gag ccc cca ccc tct cct agc ctg 332
Met Leu Leu Gly Gly Pro Gly Gln Glu Pro Pro Pro Ser Pro Ser Leu
25 30 35

gat gac tac gtg agg tct ata tct cga ctg gca cag ccc acc tct gtg 380
Asp Asp Tyr Val Arg Ser Ile Ser Arg Leu Ala Gln Pro Thr Ser Val
40 45 50

ctg gac aag gcc acg gcc cag ggc caa ccc agg cca ccc cac agg cca 428
Leu Asp Lys Ala Thr Ala Gln Gly Gln Pro Arg Pro Pro His Arg Pro
55 60 65

gcc cag gcc tgc cgg aag ggc cgc cct gct gtg tcc ctg cga gac atc 476
Ala Gln Ala Cys Arg Lys Gly Arg Pro Ala Val Ser Leu Arg Asp Ile
70 75 80 85

acc gca cgt ttc agt ggc cag cag ccc aca ctg ccc atg gct gat act 524
Thr Ala Arg Phe Ser Gly Gln Gln Pro Thr Leu Pro Met Ala Asp Thr
90 95 100

gtg gac ccc ctg gac tgg ctt ttt ggg gag tcc cag gaa aag cag cca 572
Val Asp Pro Leu Asp Trp Leu Phe Gly Glu Ser Gln Glu Lys Gln Pro
105 110 115

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Ser Gln Arg Asp Leu Pro Arg Arg Thr Gly Pro Ser Ala Gln Leu Trp
120 125 130

ggc cca cat aga cag atg gac agc aag ccc acg ggg gcc ccc aga 668
Gly Pro His Arg Gln Met Asp Ser Ser Lys Pro Thr Gly Ala Pro Arg
135 140 145

ggg agg ctc tgc gaa gcc agg atg cct ggg cat tcc ctg gca aga cca Gly Arg Leu Cys Glu Ala Arg Met Pro Gly His Ser Leu Ala Arg Pro	716
150 155 160 165	
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170 175 180	
cag tct gcc caa gcc atg gcc tcc cgc cac cgc ccc cgc ccc agc agt Gln Ser Ala Gln Ala Met Ala Ser Arg His Arg Pro Arg Pro Ser Ser	812
185 190 195	
gtc ctc aga aca ctc tac tcg cac ctc ccg gtg atc cat gaa ctc Val Leu Arg Thr Leu Tyr Ser His Leu Pro Val Ile His Glu Leu	857
200 205 210	
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aaaaaaaaaa a	1997
	2008

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Glu Thr Thr Glu Glu Met Leu Leu Gly Gly Pro Gly Gin Glu Pro Pro
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Pro Ser Pro Ser Leu Asp Asp Tyr Val Arg Ser Ile Ser Arg Leu Ala
35 40 45

Gln Pro Thr Ser Val Leu Asp Lys Ala Thr Ala Gln Gly Gln Pro Arg
50 55 60

Pro Pro His Arg Pro Ala Gln Ala Cys Arg Lys Gly Arg Pro Ala Val
65 70 75 80

Ser Leu Arg Asp Ile Thr Ala Arg Phe Ser Gly Gln Gln Pro Thr Leu
85 90 95

Pro Met Ala Asp Thr Val Asp Pro Leu Asp Trp Leu Phe Gly Glu Ser
100 105 110

Gln Glu Lys Gln Pro Ser Gln Arg Asp Leu Pro Arg Arg Thr Gly Pro
115 120 125

Ser Ala Gly Leu Trp Gly Pro His Arg Gln Met Asp Ser Ser Lys Pro
130 135 140

Thr Gly Ala Pro Arg Gly Arg Leu Cys Glu Ala Arg Met Pro Gly His
145 150 155 160

Ser Leu Ala Arg Pro Pro Gln Asp Gly Gln Gln Ser Ser Asp Leu Arg
165 170 175

Ser Trp Thr Phe Gly Gln Ser Ala Gln Ala Met Ala Ser Arg His Arg
180 185 190

Pro Arg Pro Ser Ser Val Leu Arg Thr Leu Tyr Ser His Leu Pro Val
195 200 205

Ile His Glu Leu
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agcagccccc cgaggcctga ccaaccgcga ggaccggcgg aggagccccc cctggatgtc 360
aagcgg atg cca agc gga tgc cac agt tcc ccc ccc agc gga ctc cgt 408
Met Pro Ser Gly Cys His Ser Ser Pro Pro Ser Gly Leu Arg
1 5 10

ggg gac atg gct tcg ctg gtg ccc ctt tcc cca tat cta agc ccc acg 456
Gly Asp Met Ala Ser Leu Val Pro Leu Ser Pro Tyr Leu Ser Pro Thr
15 20 25 30

gtc ctc ctg gtc agc tgt gac ctg ggc ttc gtg cga gca gac cgg Val Leu Leu Leu Val Ser Cys Asp Leu Gly Phe Val Arg Ala Asp Arg 35 40 45	504
cct ccc tct cct gtg aat gtg acg gtc act cac ctc aga gcc aac tcc Pro Pro Ser Pro Val Asn Val Thr Val Thr His Leu Arg Ala Asn Ser 50 55 60	552
gcc act gtg tcc tgg gac gtc cca gaa ggc aac atc gtc att ggc tac Ala Thr Val Ser Trp Asp Val Pro Glu Gly Asn Ile Val Ile Gly Tyr 65 70 75	600
tcc att tcc cag caa cgg cag aat ggc ccc ggg cag cgt gtg att cgg Ser Ile Ser Gln Gln Arg Gln Asn Gly Pro Gly Gln Arg Val Ile Arg 80 85 90	648
gag gtg aac acc acc cgg gcc tgt gcc ctc tgg ggc ctg gct gaa Glu Val Asn Thr Thr Arg Ala Cys Ala Leu Trp Gly Leu Ala Glu 95 100 105 110	696
gac agt gac tac aca gtg cag gtc agg agc atc ggc ctt cgg gga gag Asp Ser Asp Tyr Thr Val Gln Val Arg Ser Ile Gly Leu Arg Gly Glu 115 120 125	744
agt ccc cca ggg ccc cgg gtg cac ttc cga act ctc aag ggt tct gac Ser Pro Pro Gly Pro Arg Val His Phe Arg Thr Leu Lys Gly Ser Asp 130 135 140	792
cgg cta cct tca aac agt tca agc cca ggt gac atc aca gtg gaa ggt Arg Leu Pro Ser Asn Ser Ser Pro Gly Asp Ile Thr Val Glu Gly 145 150 155	840
ctg gat gga gag cgg cca ctg cag act ggg gaa gtg gtc atc att gtg Leu Asp Gly Glu Arg Pro Leu Gin Thr Gly Glu Val Val Ile Ile Val 160 165 170	888
gtg gtg ttg ctc atg tgg gct gct gta att ggg ctg ttc tgc cgt cag Val Val Leu Leu Met Trp Ala Ala Val Ile Gly Leu Phe Cys Arg Gln 175 180 185 190	936
tat gac atc atc aag gac aat gac tcc aac aac aat ccc aag gag aag Tyr Asp Ile Ile Lys Asp Asn Asp Ser Asn Asn Asn Pro Lys Glu Lys 195 200 205	984
gga aag ggg ccg gaa cag agt cct cag gga agg cca gtg ggg aca aga Gly Lys Gly Pro Glu Gln Ser Pro Gln Gly Arg Pro Val Gly Thr Arg 210 215 220	1032
cag aaa aag tca cca tct atc aac acc atc gac gtt tgagtgaaga Gln Lys Lys Ser Pro Ser Ile Asn Thr Ile Asp Val 225 230	1078
aacacaccca gaagagagat gcactaacaa ctggggatag ggatgggtc agggggagcc caagatggtg atctggccga gactccaga ggtaatgcc actcccacaa totcaggcc ggtacccatc ctcttccac tgtgagcaga gccagaaggt aggtctgtc agagtctgt ccccctggacc tggggagtgg atatcagatg ggatatctcc ttccattccc cggtccaggg gagagtcact agttgtaccc tactccatta ggtcccaa at gggggccca tttcacctgt atcaggactc tgagcatccc cagtcgcccc acatctgcc tctggccctc agagaggg gtttctgtgg gtactccctc taccggcaga aataaaagga atttgtctgac cctagaggca gtatgtgcac tgcactactc caatgtcttc catggagcct caggtgtcc ccctctcacc tggcagcccc tttagtgcgt agtgatataca ctgttggac atttttccaa taaagggttct ttggacaaaaact ggaaaaaaaaaaa a	1138 1198 1258 1318 1378 1438 1498 1558 1618 1649

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<212> PRT

<213> Homo sapiens

<400> 20

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Met Ala Ser Leu Val Pro Leu Ser Pro Tyr Leu Ser Pro Thr Val Leu
20 25 30

Leu Leu Val Ser Cys Asp Leu Gly Phe Val Arg Ala Asp Arg Pro Pro
35 40 45

Ser Pro Val Asn Val Thr Val Thr His Leu Arg Ala Asn Ser Ala Thr
50 55 60

Val Ser Trp Asp Val Pro Glu Gly Asn Ile Val Ile Gly Tyr Ser Ile
65 70 75 80

Ser Gln Gln Arg Gln Asn Gly Pro Gly Gln Arg Val Ile Arg Glu Val
85 90 95

Asn Thr Thr Thr Arg Ala Cys Ala Leu Trp Gly Leu Ala Glu Asp Ser
100 105 110

Asp Tyr Thr Val Gln Val Arg Ser Ile Gly Leu Arg Gly Glu Ser Pro
115 120 125

Pro Gly Pro Arg Val His Phe Arg Thr Leu Lys Gly Ser Asp Arg Leu
130 135 140

Pro Ser Asn Ser Ser Ser Pro Gly Asp Ile Thr Val Glu Gly Leu Asp
145 150 155 160

Gly Glu Arg Pro Leu Gln Thr Gly Glu Val Val Ile Ile Val Val Val
165 170 175

Leu Leu Met Trp Ala Ala Val Ile Gly Leu Phe Cys Arg Gln Tyr Asp
180 185 190

Ile Ile Lys Asp Asn Asp Ser Asn Asn Asn Pro Lys Glu Lys Gly Lys
195 200 205

Gly Pro Glu Gln Ser Pro Gln Gly Arg Pro Val Gly Thr Arg Gln Lys
210 215 220

Lys Ser Pro Ser Ile Asn Thr Ile Asp Val
225 230

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<212> DNA

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ttcctgagga cgtggagaaa actttctgt gagaaggaca tttgaaggt ttgttggtct	180
gaaaaaactg ttcttggaaat cacccttaga tctttcttga agacttgaat tagattacag	240
cg atg ggg aca cag aag gtc acc cca gct ctg ata ttt gcc atc aca Met Gly Thr Gln Lys Val Thr Pro Ala Leu Ile Phe Ala Ile Thr	287
1 5 10 15	
gtt gct aca atc ggc tct ttc caa ttt ggc tac aac act ggg gtc atc Val Ala Thr Ile Gly Ser Phe Gln Phe Gly Tyr Asn Thr Gly Val Ile	335
20 25 30	
aat got cct gag aag atc ata aag gaa ttt atc aat aaa act ttg acg Asn Ala Pro Glu Lys Ile Ile Lys Glu Phe Ile Asn Lys Thr Leu Thr	383
35 40 45	
gac aag gga aat gcc cca ccc tct gag gtg ctg ctc acg tct ctc tgg Asp Lys Gly Asn Ala Pro Pro Ser Gln Val Leu Leu Thr Ser Leu Trp	431
50 55 60	
tcc ttg tct gtg gcc ata ttt tcc gtc ggg ggt atg atc ggc tcc ttt Ser Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser Phe	479
65 70 75	
tcc gtc gga ctc ttc gtc aac cgc ttt ggc agg cgc aat tca atg ctg Ser Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met Leu	527
80 85 90 95	
att gtc aac ctg ttg gct gtc act ggt ggc tgc ttt atg gga ctg tgt Ile Val Asn Leu Leu Ala Val Thr Gly Gly Cys Phe Met Gly Leu Cys	575
100 105 110	
aaa gta gct aag tcg gtt gaa atg ctg atc ctg ggt cgc ttg gtt att Lys Val Ala Lys Ser Val Glu Met Leu Ile Leu Gly Arg Leu Val Ile	623
115 120 125	
ggc ctc ttc tgc gga ctc tgc aca ggt ttt gtg ccc atg tac att gga Gly Leu Phe Cys Gly Leu Cys Thr Gly Phe Val Pro Met Tyr Ile Gly	671
130 135 140	
gag atc tcg cct act gcc ctg cgg ggt gcc ttt ggc act ctc aac cag Glu Ile Ser Pro Thr Ala Leu Arg Gly Ala Phe Gly Thr Leu Asn Gln	719
145 150 155	
ctg ggc atc gtt gtt gga att ctg gtg gcc cag atc ttt ggt ctg gaa Leu Gly Ile Val Val Gly Ile Leu Val Ala Gln Ile Phe Gly Leu Glu	767
160 165 170 175	
ttc atc ctt ggg tct gaa gag cta tgg cog ctg cta ctg ggt ttt acc Phe Ile Leu Gly Ser Glu Glu Leu Trp Pro Leu Leu Leu Gly Phe Thr	815
180 185 190	
atc ctt cct gct atc cta caa agt gca gcc ctt cca ttt tgc cct gaa Ile Leu Pro Ala Ile Leu Gln Ser Ala Ala Leu Pro Phe Cys Pro Glu	863
195 200 205	
agt ccc aga ttt ttg ctc att aac aga aaa gaa gag gag aat gct aag Ser Pro Arg Phe Leu Leu Ile Asn Arg Lys Glu Glu Glu Asn Ala Lys	911
210 215 220	
cag atc ctc cag cgg ttg tgg ggc acc cag gat gta tcc caa gac atc Gln Ile Leu Gln Arg Leu Trp Gly Thr Gln Asp Val Ser Gln Asp Ile	959
225 230 235	
cag gag atg aaa gat gag agt gca agg atg tca caa gaa aag caa gtc Gln Glu Met Lys Asp Glu Ser Ala Arg Met Ser Gln Glu Lys Gln Val	1007
240 245 250 255	
acc gtg cta gag ctc ttt aga gtg tcc agc tac cga cag ccc atc atc Thr Val Leu Glu Leu Phe Arg Val Ser Ser Tyr Arg Gln Pro Ile Ile	1055
260 265 270	
att tcc att gtg ctc cag ctc tct cag cag ctc tct ggg atc aat gct	1103

Ile Ser Ile Val Leu Gin Leu Ser Gin Gin Leu Ser Gly Ile Asn Ala			
275	280	285	
gtg ttc tat tac tca aca gga atc ttc aag gat gca ggt gtt caa gag	1151		
Val Phe Tyr Tyr Ser Thr Gly Ile Phe Lys Asp Ala Gly Val Gin Glu			
290	295	300	
ccc atc tat gcc acc atc ggc gcg ggt gtg gtt aat act atc ttc act	1199		
Pro Ile Tyr Ala Thr Ile Gly Ala Gly Val Val Asn Thr Ile Phe Thr			
305	310	315	
gta gtt tct cta ttt ctg gtg gaa agg gca gga aga agg act ctg cat	1247		
Val Val Ser Leu Phe Leu Val Glu Arg Ala Gly Arg Arg Thr Leu His			
320	325	330	335
atg ata ggc ctt gga ggg atg gct ttt tgt tcc acg ctc atg act gtt	1295		
Met Ile Gly Leu Gly Gly Met Ala Phe Cys Ser Thr Leu Met Thr Val			
340	345	350	
tct ttg tta tta aag gat aac tat aat ggg atg agc ttt gtc tgt att	1343		
Ser Leu Leu Leu Lys Asp Asn Tyr Asn Gly Met Ser Phe Val Cys Ile			
355	360	365	
ggg gct atc ttg gtc ttt gta gcc ttc ttt gaa att gga cca ggc ccc	1391		
Gly Ala Ile Leu Val Phe Val Ala Phe Phe Glu Ile Gly Pro Gly Pro			
370	375	380	
att ccc tgg ttt att gtg gcc gaa ctc ttc agc cag ggc ccc cgc cca	1439		
Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro			
385	390	395	
gct gcg atg gca gtg gcc ggc tgc tcc aac tgg acc tcc aac ttc cta	1487		
Ala Ala Met Ala Val Ala Gly Cys Ser Asn Trp Thr Ser Asn Phe Leu			
400	405	410	415
gtc gga ttg ctc ttc ccc tcc gct gct cac tat tta gga gcc tac gtt	1535		
Val Gly Leu Leu Phe Pro Ser Ala Ala His Tyr Leu Gly Ala Tyr Val			
420	425	430	
ttt att atc ttc acc ggc ttc ctc att acc ttc ttg gct ttt acc ttc	1583		
Phe Ile Ile Phe Thr Gly Phe Leu Ile Thr Phe Leu Ala Phe Thr Phe			
435	440	445	
ttc aaa gtc cct gag acc cgt ggc agg act ttt gag gat atc aca cgg	1631		
Phe Lys Val Pro Glu Thr Arg Gly Arg Thr Phe Glu Asp Ile Thr Arg			
450	455	460	
gcc ttt gaa ggg cag gca cac ggt gca gat aga tct gga aag gac ggc	1679		
Ala Phe Glu Gly Gin Ala His Gly Ala Asp Arg Ser Gly Lys Asp Gly			
465	470	475	
gtc atg gag atg aac agc atc gag cct gct aag gag acc acc acc aat	1727		
Val Met Glu Met Asn Ser Ile Glu Pro Ala Lys Glu Thr Thr Thr Asn			
480	485	490	495
gtc taagtctgtgc ctccctccac ctccctcccc gcatggaaaa gccacctctc	1780		
Val			
cctcaacaag ggagagacct catcaggatg aaccaggac gtttctaat gctgctactt	1840		
aattcccttc tcatccccacg cactccatga gcaccccaag gtcgcgttt gttggatctt	1900		
caatggctt ttaaatttta ttccctggac atccctttct gtttaggaga gaccgagtga	1960		
acctaccccttc atttcaggag ggattggccg cttggcacat gacaactttt ccagctttc	2020		
ctcccttggg ttctgatatt gcccactag gggatataagg agaggaaaag taaggtcag	2080		
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gatacatgtg ccgaatgtgc aggtttgtta cataggtata tatatgccat gatggaaata	2320		

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ataagaattt agggagaaat	gttgttcatt attggaggtt	aatgatgtg gtgcctgagg	2500
tctgtacgtt acctcttaac	aatttctgtc cttcagatgg	aaactctta acttctcgta	2560
aaagtcatat acctatataa	taaagctact gatttcctt	gagctttttt cttaagata	2620
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gaaaggctgt tcccctact	ggatgaaata	actccttctt gttagtgc当地	2800
gaagtaatcc cgccacctat	ctcgtggag	agccatccaa ataagaaacc	2860
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ttttctgtt tattttact	catacctta	aaggaattcc ccaaagaatg	2980
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atgtgttgt tgctttagc	tcacggcacg	cttgc当地 tctgttacca	3100
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atgagtcaat gtgc当地gt	gcccacactt	gagaggatga atgtatgtc	3220
tgc当地tgggt ggaagtacgt	tatttgcac	actgtcactt	3280
cTTTCTCATA ttttgc当地	tctcccttc	cottcttggt gcttacacat	3340
ttagccaaac ctttgc当地	gacagtattt	tggttcttag	3400
cctggagcct ttgaataaaa	atgc当地gt	ctgaggccgg atgc当地gtc	3460
aatcccagca ctttggagg	cctaggccgg	cggtcagggg	3520
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ctgtatccc agctacttgg	gaagctgagg	cgggagaatc	3640
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ttgcaacttc atgtcaactt	tctggctcct	ggccacagg	3820
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 <211> 496
 <212> PRT
 <213> Homo sapiens
 <400> 22

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Ala Thr Ile Gly Ser Phe Gln Phe Gly Tyr Asn Thr Gly Val Ile Asn
 20 25 30

Ala Pro Glu Lys Ile Ile Lys Glu Phe Ile Asn Lys Thr Leu Thr Asp
 35 40 45

Lys Gly Asn Ala Pro Pro Ser Glu Val Leu Leu Thr Ser Leu Trp Ser

50

55

60

Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser Phe Ser
 65 70 75 80

Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met Leu Ile
 85 90 95

Val Asn Leu Leu Ala Val Thr Gly Gly Cys Phe Met Gly Leu Cys Lys
 100 105 110

Val Ala Lys Ser Val Glu Met Leu Ile Leu Gly Arg Leu Val Ile Gly
 115 120 125

Leu Phe Cys Gly Leu Cys Thr Gly Phe Val Pro Met Tyr Ile Gly Glu
 130 135 140

Ile Ser Pro Thr Ala Leu Arg Gly Ala Phe Gly Thr Leu Asn Gln Leu
 145 150 155 160

Gly Ile Val Val Gly Ile Leu Val Ala Gln Ile Phe Gly Leu Glu Phe
 165 170 175

Ile Leu Gly Ser Glu Glu Leu Trp Pro Leu Leu Leu Gly Phe Thr Ile
 180 185 190

Leu Pro Ala Ile Leu Gln Ser Ala Ala Leu Pro Phe Cys Pro Glu Ser
 195 200 205

Pro Arg Phe Leu Leu Ile Asn Arg Lys Glu Glu Glu Asn Ala Lys Gln
 210 215 220

Ile Leu Gln Arg Leu Trp Gly Thr Gln Asp Val Ser Gln Asp Ile Gln
 225 230 235 240

Glu Met Lys Asp Glu Ser Ala Arg Met Ser Gln Glu Lys Gln Val Thr
 245 250 255

Val Leu Glu Leu Phe Arg Val Ser Ser Tyr Arg Gln Pro Ile Ile Ile
 260 265 270

Ser Ile Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn Ala Val
 275 280 285

Phe Tyr Tyr Ser Thr Gly Ile Phe Lys Asp Ala Gly Val Gln Glu Pro
 290 295 300

Ile Tyr Ala Thr Ile Gly Ala Gly Val Val Asn Thr Ile Phe Thr Val
 305 310 315 320

Val Ser Leu Phe Leu Val Glu Arg Ala Gly Arg Arg Thr Leu His Met
 325 330 335

Ile Gly Leu Gly Gly Met Ala Phe Cys Ser Thr Leu Met Thr Val Ser
 340 345 350

Leu Leu Leu Lys Asp Asn Tyr Asn Gly Met Ser Phe Val Cys Ile Gly

355

360

365

Ala Ile Leu Val Phe Val Ala Phe Phe Glu Ile Gly Pro Gly Pro Ile
 370 375 380

Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro Ala
 385 390 395 400

Ala Met Ala Val Ala Gly Cys Ser Asn Trp Thr Ser Asn Phe Leu Val
 405 410 415

Gly Leu Leu Phe Pro Ser Ala Ala His Tyr Leu Gly Ala Tyr Val Phe
 420 425 430

Ile Ile Phe Thr Gly Phe Leu Ile Thr Phe Leu Ala Phe Thr Phe Phe
 435 440 445

Lys Val Pro Glu Thr Arg Gly Arg Thr Phe Glu Asp Ile Thr Arg Ala
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Phe Glu Gly Gln Ala His Gly Ala Asp Arg Ser Gly Lys Asp Gly Val
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Met Glu Met Asn Ser Ile Glu Pro Ala Lys Glu Thr Thr Thr Asn Val
 485 490 495

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 <212> DNA
 <213> Homo sapiens

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 <222> (76)..(678)

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 cttttttccc cagac atg gcc aac aag ggt cct tcc tat ggc atg agc cgc
 Met Ala Asn Lys Gly Pro Ser Tyr Gly Met Ser Arg 111
 1 5 10

gaa gtg cag tcc aaa atc gag aag aat gac gag gag ctg gag gag 159
 Glu Val Gin Ser Lys Ile Glu Lys Lys Tyr Asp Glu Glu Leu Glu Glu
 15 20 25

cgg ctg gtg gag tgg atc ata gtg cag tgt ggc cct gat gtg ggc cgc 207
 Arg Leu Val Glu Trp Ile Val Gln Cys Gly Pro Asp Val Gly Arg
 30 35 40

cca gac cgt ggg ccc ttg ggc ttc cag gtg tgg ctg aag aat ggc gtg 255
 Pro Asp Arg Gly Pro Leu Gly Phe Gln Val Trp Leu Lys Asn Gly Val
 45 50 55 60

att ctg agc aag ctg gtg aac agc ctg tac cct gat ggc tcc aag ccg 303
 Ile Leu Ser Lys Leu Val Asn Ser Leu Tyr Pro Asp Gly Ser Lys Pro
 65 70 75

gtg aag gtg ccc gag aac cca ccc tcc atg gtc ttc aag cag atg gag 351
 Val Lys Val Pro Glu Asn Pro Pro Ser Met Val Phe Lys Gln Met Glu
 80 85 90

cag gtg gct cag ttc ctg aag gcg gct gag gac tct ggg gtc atc aag 399
 Gln Val Ala Gln Phe Leu Lys Ala Ala Glu Asp Ser Gly Val Ile Lys
 95 100 105

act gac atg ttc cag act gtt gac ctc ttt gaa ggc aaa gac atg gca Thr Asp Met Phe Gin Thr Val Asp Leu Phe Glu Gly Lys Asp Met Ala	447
110 115 120	
gca gtg cag agg acc ctg atg gct ttg ggc agc ttg gca gtg acc aag Ala Val Gin Arg Thr Leu Met Ala Leu Gly Ser Leu Ala Val Thr Lys	495
125 130 135 140	
aat gat ggg cac tac cgt gga gat ccc aac tgg ttt atg aag aaa gcg Asn Asp Gly His Tyr Arg Gly Asp Pro Asn Trp Phe Met Lys Lys Ala	543
145 150 155	
cag gag cat aag agg gaa ttc aca gag agc cag ctg cag gag gga aag Gln Glu His Lys Arg Glu Phe Thr Glu Ser Gln Leu Gln Glu Gly Lys	591
160 165 170	
cat gtc att ggc ctt cag atg ggc agc aac aga ggg gcc tcc cag gcc His Val Ile Gly Leu Gln Met Gly Ser Asn Arg Gly Ala Ser Gln Ala	639
175 180 185	
ggc atg aca ggc tac gga cga cct cgg cag atc atc atc agt tagagcggag Gly Met Thr Gly Tyr Gly Arg Pro Arg Gln Ile Ile Ser	688
190 195 200	
aggcctagcc ctgagccccc cgctccccca gctccttggc tgccagccatc ccgccttagcc tgccctcaccc acaccgggt ggtacccctca gcccctggcca agctttgagg ctctgtca	748
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<210> 24
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<400> 24

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Lys Ile Glu Lys Lys Tyr Asp Glu Glu Leu Glu Arg Leu Val Glu
20 25 30

Trp Ile Ile Val Gln Cys Gly Pro Asp Val Gly Arg Pro Asp Arg Gly
35 40 45

Pro Leu Gly Phe Gln Val Trp Leu Lys Asn Gly Val Ile Leu Ser Lys
50 55 60

Leu Val Asn Ser Leu Tyr Pro Asp Gly Ser Lys Pro Val Lys Val Pro
65 70 75 80

Glu Asn Pro Pro Ser Met Val Phe Lys Gln Met Glu Gln Val Ala Gln
85 90 95

Phe Leu Lys Ala Ala Glu Asp Ser Gly Val Ile Lys Thr Asp Met Phe
100 105 110

Gln Thr Val Asp Leu Phe Glu Gly Lys Asp Met Ala Ala Val Gln Arg
115 120 125

Thr Leu Met Ala Leu Gly Ser Leu Ala Val Thr Lys Asn Asp Gly His
130 135 140

Tyr Arg Gly Asp Pro Asn Trp Phe Met Lys Lys Ala Gln Glu His Lys
145 150 155 160

Arg Glu Phe Thr Glu Ser Gln Leu Gln Glu Gly Lys His Val Ile Gly
165 170 175

Leu Gln Met Gly Ser Asn Arg Gly Ala Ser Gln Ala Gly Met Thr Gly
180 185 190

Tyr Gly Arg Pro Arg Gln Ile Ile Ser
195 200

<210> 25

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Oligonucleotide designed to act as primer for amplifying kiaa1001 gene transcript.

<400> 25

ggaacatctc tttaatttgtt attttttgtt 30

<210> 26

<211> 22

<212> DNA

<213> Artificial

<220>

<223> Oligonucleotide designed to act as primer for amplifying kiaa1001 gene transcript.

<400> 26

agccacagcc aaaaaagact tt 22

<210> 27

<211> 32

<212> DNA

<213> Artificial

<220>

<223> Oligonucleotide designed to act as TaqMan probe for detecting amplification of kiaa1001 gene transcript.

<400> 27

ttacatactt agagagagac tcttttagcc ag 32

<210> 28

<211> 28

<212> DNA

<213> Artificial

<220>

<223> Oligonucleotide designed to act as primer for amplifying asah1 gene transcript.

<400> 28

accctaagga agttgctaac ttaaaaaaa 28

<210> 29

<211> 29

<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying asah1 gene transcript.

<400> 29
tccacaagtc tttgacttgt ttatTTACT 29

<210> 30
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as TaqMan probe for detecting amplification of asah1 gene transcript.

<400> 30
ctgcatccc cgttctgtta att 23

<210> 31
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying mgc4171 gene transcript.

<400> 31
cagggtgtct tttggtgcc ta 22

<210> 32
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying mgc4171 gene transcript.

<400> 32
agtggctccc acgctgaa 18

<210> 33
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as TaqMan probe for detecting amplification of mgc4171 gene transcript.

<400> 33
tgaagagtcg gattttgaag cagc 24

<210> 34
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying lss gene transcript.

<400> 34
gtccgggtgc tacttgagaa acag 24

<210> 35
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying lss gene transcript.

<400> 35
agaccccaagc aatgttttcc t 21

<210> 36
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as TaqMan probe for detecting amplification of lss gene transcript.

<400> 36
cccaatggcg actggccg 18

<210> 37
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying nr0b2 gene transcript.

<400> 37
cagcacttgg ctcccttagga a 21

<210> 38
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying nr0b2 gene transcript.

<400> 38
actgtgtcca aaccaggaa gtc 23

<210> 39
<211> 23
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<400> 39
agctcttcac tcagccacac ccc 23

<210> 40
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<220>
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gagtttctcc ggcaagtacc aa 22

<210> 41
<211> 20
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<220>
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<400> 41
cagaccgatt gccttcatga 20

<210> 42
<211> 25
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<213> Artificial

<220>
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<400> 42
tgcagagcca gaaaaacttt gaagc 25

<210> 43
<211> 22
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<220>
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gaaaccagat caagcccaag at 22

<210> 44
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ccctggcagg catcaatg 18

<210> 45
<211> 20
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<400> 45
ttctgtgctg gctaccccg 20

<210> 46
<211> 21
<212> DNA
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<220>
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<400> 46
gaggagggca cagaaggcatc t 21

<210> 47
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<220>
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<400> 47
ccttgcgtcc actaatgcag aaag 24

<210> 48
<211> 24
<212> DNA
<213> Artificial

<220>
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<400> 48
tgccacagca gtcaaaatca ccct 24

<210> 49
<211> 20
<212> DNA
<213> Artificial

<220>
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<400> 49
tgtgggtggca ttgggagagt 20

<210> 50
<211> 25
<212> DNA
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<220>
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tggtagcact gagtggtaca gattc 25

<210> 51
<211> 22
<212> DNA
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<220>
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<400> 51
cccccatgtat gagggccaag at 22

<210> 52
<211> 22
<212> DNA
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<220>
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gene transcript.

<400> 52
ggtaatgcca ctccccacaat ct 22

<210> 53
<211> 21
<212> DNA
<213> Artificial

<220>
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<400> 53
ccttctggct ctgtcacag t 21

<210> 54
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<212> DNA
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<220>
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aggccctggta cccatccctct ttc 23

<210> 55
<211> 21
<212> DNA
<213> Artificial

<220>
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gcttgaaaag gtgacaccttgc a 21

<210> 56
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying slc2a3 gene transcript.

<400> 56
tgccttactg ccaacctact gtt 23

<210> 57
<211> 23
<212> DNA
<213> Artificial

<220>
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<400> 57
tcatgtcaac ttctggctc ctc 23

<210> 58
<211> 25
<212> DNA
<213> Artificial

<220>
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gene transcript.

<400> 58
gagcataaga gggaattcac agaga 25

<210> 59
<211> 20
<212> DNA
<213> Artificial

<220>
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gene transcript.

<400> 59
ctgttgctgc ccatctgaag 20

<210> 60
<211> 27
<212> DNA
<213> Artificial

<220>
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amplification of tagln gene transcript.

<400> 60
agctgcagga gggaaagcat gtcattg 27